

POLAR DIVERSITY OF THE TARDIGRADA: A COMBINED MORPHOLOGICAL / MOLECULAR APPROACH

C.J. Sands¹, S.J. McInnes¹, N.J. Marley², W.P. Goodall-Copestake¹, P. Convey¹, L. Linse¹

1 - Natural Environment Research Council, British Antarctic Survey, High Cross, Madingley Road, Cambridge, CB3 0ET, United Kingdom

2 - Marine Biology and Ecology Research Centre, University of Plymouth, Drake Circus, Plymouth, PL4 8AA, United Kingdom

cjsan@bas.ac.uk

Examining the spatial distributions of organisms can provide information regarding their evolutionary history. We are investigating the origins and the processes that influence the contemporary distribution and diversity of Antarctic terrestrial biota. Tardigrades were chosen as a model group, as representatives are found in a diverse range of habitats across the Antarctic continent and sub-Antarctic islands. Our investigations involving approximately 400 individuals and 3 genes have identified systematic complexity requiring attention in order to prevent confounding the biogeographic signal. To overcome the challenges inherent in taxonomic and molecular work on very tiny animals (meiofauna), we have developed a protocol that allows efficient sample extraction and identification without interfering with downstream molecular processes. Our protocol provides joint morphological/molecular assessment of tardigrade taxonomy at the level of the individual that has resulted in identification of numerous cryptic species, cryptic genera and even cryptic families. To resolve polyphyly at the family level we have proposed three superfamilies that are strongly supported by molecular analyses. Here we present a systematic revision of the phylum Tardigrada along with some novel insights regarding Antarctic tardigrade biogeography.